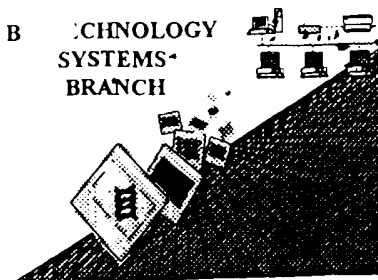


RAW SEQUENCE LISTING ERROR REPORT

B IOTECHNOLOGY
SYSTEMS
BRANCH



CB

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/806703
Source: PCT
Date Processed by STIC: 08/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1 821 - 1 825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/806703

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
 <210> sequence id number
 <400> sequence id number
 000
- 9 ✓ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors

PCT09

RAW SEQUENCE LISTING

DATE: 08/30/2001

PATENT APPLICATION: US/09/806,703

TIME: 09:49:05

Input Set : A:\3631-109P.ST25.txt

Output Set: N:\CRF3\08302001\I806703.raw

3 <110> APPLICANT: Steinaa, Lucilla
 4 Mouritsen, Soren
 5 Gautam, Anand
 6 Dalum, Iben
 7 Haaning, Jesper
 8 Leach, Dana
 9 Nielsen, Klaus
 10 Karlsson, Gunilla
 11 Rasmussen, Peter
 13 <120> TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
 15 <130> FILE REFERENCE: 3631-109P
 17 <140> CURRENT APPLICATION NUMBER: US 09/806,703
 18 <141> CURRENT FILING DATE: 2001-04-04
 20 <150> PRIOR APPLICATION NUMBER: PCT/DK99/00525
 21 <151> PRIOR FILING DATE: 1999-10-05
 23 <150> PRIOR APPLICATION NUMBER: DK 1998 01261
 24 <151> PRIOR FILING DATE: 1998-10-05
 26 <150> PRIOR APPLICATION NUMBER: DK 60/105,011
 27 <151> PRIOR FILING DATE: 1998-10-20
 29 <160> NUMBER OF SEQ ID NOS: 33
 31 <170> SOFTWARE: PatentIn version 3.0
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 2253
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Homo sapiens
 38 <220> FEATURE:
 39 <221> NAME/KEY: CDS
 40 <222> LOCATION: (1)..(2253)
 42 <220> FEATURE:
 43 <221> NAME/KEY: misc_feature
 44 <222> LOCATION: (58)..(2253)
 45 <223> OTHER INFORMATION: Human PSM'
 48 <400> SEQUENCE: 1
 49 atg kgk aat ctc ctt cac gaa acc gac tcg gct gtg gcc acc gcg cgc 48
 50 Met Xaa Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
 51 1 5 10 15
 53 cgc ccg cgc tgg ctg tgc gct ggg gcg ctg gtg ctg gcg ggt ggc ttc 96
 54 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
 55 20 25 30
 57 ttt ctc ctc ggc ttc ctc ttc ggg tgg ttt ata aaa tcc tcc aat gaa 144
 58 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
 59 35 40 45
 61 gct act aac att act cca aag cat aat atg aaa gca ttt ttg gat gaa 192
 62 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
 63 50 55 60
 65 ttg aaa gct gag aac atc aag aag ttc tta tat aat ttt aca cag ata 240
 66 Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile

DATE: 08/30/2001

TIME: 09:49:05

Output Set: N:\CRF3\08302001\I806703.raw

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,703

DATE: 08/30/2001

TIME: 09:49:05

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Output Set: N:\CRF3\08302001\I806703.raw

133	ttt	tct	aca	caa	aaa	gtc	aag	atg	cac	atc	cac	tct	acc	aat	gaa	gtg	1056
134	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Thr	Asn	Glu	Val	
135				340					345					350			
137	aca	aga	att	tac	aat	gtg	ata	ggt	act	ctc	aga	gga	gca	gtg	gaa	cca	1104
138	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	
139			355					360					365				
141	gac	aga	tat	gtc	att	ctg	gga	ggt	cac	cgg	gac	tca	tgg	gtg	ttt	ggt	1152
142	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	
143		370					375					380					
145	ggt	att	gac	cct	cag	agt	gga	gca	gct	ggt	ggt	cat	gaa	att	gtg	agg	1200
146	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg	
147	385					390					395					400	
149	agc	ttt	gga	aca	ctg	aaa	aag	gaa	ggg	tgg	aga	cct	aga	aga	aca	att	1248
150	Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile	
151				405					410						415		
153	ttg	ttt	gca	agc	tgg	gat	gca	gaa	gaa	ttt	ggt	ctt	ctt	ggt	tct	act	1296
154	Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr	
155			420					425					430				
157	gag	tgg	gca	gag	gag	aat	tca	aga	ctc	ctt	caa	gag	cgt	ggc	gtg	gct	1344
158	Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala	
159			435				440					445					
161	tat	att	aat	gct	gac	tca	tct	ata	gaa	gga	aac	tac	act	ctg	aga	gtt	1392
162	Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val	
163		450				455					460						
165	gat	tgt	aca	ccg	ctg	atg	tac	agc	ttg	gta	cac	aac	cta	aca	aaa	gag	1440
166	Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu	
167	465				470				475						480		
169	ctg	aaa	agc	cct	gat	gaa	ggc	ttt	gaa	ggc	aaa	tct	ctt	tat	gaa	agt	1488
170	Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu	Ser	
171				485					490					495			
173	tgg	act	aaa	aaa	agt	cct	tcc	cca	gag	ttc	agt	ggc	atg	ccc	agg	ata	1536
174	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	Arg	Ile	
175			500						505				510				
177	agc	aaa	ttg	gga	tct	gga	aat	gat	ttt	gag	gtg	ttc	ttc	caa	cga	ctt	1584
178	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	Gln	Arg	Leu	
179			515				520					525					
181	gga	att	gct	tca	ggc	aga	gca	cgg	tat	act	aaa	aat	tgg	gaa	aca	aac	1632
182	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Glu	Thr	Asn	
183		530				535						540					
185	aaa	ttc	agc	ggc	tat	cca	ctg	tat	cac	agt	gtc	tat	gaa	aca	tat	gag	1680
186	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val	Tyr	Glu	Thr	Tyr	Glu	
187	545				550					555					560		
189	ttg	gtg	gaa	aag	ttt	tat	gat	cca	atg	ttt	aaa	tat	cac	ctc	act	gtg	1728
190	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe	Lys	Tyr	His	Leu	Thr	Val	
191				565					570					575			
193	gcc	cag	gtt	cga	gga	ggg	atg	gtg	ttt	gag	cta	gcc	aat	tcc	ata	gtg	1776
194	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser	Ile	Val	
195			580						585				590				
197	ctc	cct	ttt	gat	tgt	cga	gat	tat	gct	gta	gtt	tta	aga	aag	tat	gct	1824

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,703

DATE: 08/30/2001

TIME: 09:49:05

Input Set : A:\3631-109P.ST25.txt

Output Set: N:\CRF3\08302001\I806703.raw

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198 Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
199          595          600          605
201 gac aaa atc tac agt att tct atg aaa cat cca cag gaa atg aag aca      1872
202 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
203      610          615          620
205 tac agt gta tca ttt gat tca ctt ttt tct gca gta aag aat ttt aca      1920
206 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
207 625          630          635          640
209 gaa att gct tcc aag ttc agt gag aga ctc cag gac ttt gac aaa agc      1968
210 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
211          645          650          655
213 aac cca ata gta tta aga atg atg aat gat caa ctc atg ttt ctg gaa      2016
214 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
215          660          665          670
217 aga gca ttt att gat cca tta ggg tta cca gac agg cct ttt tat agg      2064
218 Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
219          675          680          685
221 cat gtc atc tat gct cca agc agc cac aac aag tat gca ggg gag tca      2112
222 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
223      690          695          700
225 ttc cca gga att tat gat gct ctg ttt gat att gaa agc aaa gtg gac      2160
226 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
227 705          710          715          720
229 cct tcc aag gcc tgg gga gaa gtg aag aga cag att tat gtt gca gcc      2208
230 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
231          725          730          735
233 ttc aca gtg cag gca gct gca gag act ttg agt gaa gta gcc taa      2253
234 Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
235          740          745          750

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238 <210> SEQ ID NO: 2

239 <211> LENGTH: 750

240 <212> TYPE: PRT

241 <213> ORGANISM: Homo sapiens

243 <220> FEATURE:

244 <221> NAME/KEY: misc_feature

245 <222> LOCATION: (58)..(2253)

246 <223> OTHER INFORMATION: Human PSM'

248 <400> SEQUENCE: 2

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W--> 250 Met Xaa Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
251 1          5          10          15
254 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
255          20          25          30
258 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
259          35          40          45
262 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
263          50          55          60
266 Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
267 65          70          75          80
270 Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile

```

- Error: When unknowns are included
in a sequence listing, they must be
enumerated in fields 221, 222, 223.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,703

DATE: 08/30/2001

TIME: 09:49:05

Input Set : A:\3631-109P.ST25.txt

Output Set: N:\CRF3\08302001\I806703.raw

271				85				90				95				
274	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	Asp	Ser	Val	Glu	Leu	Ala	His
275				100					105					110		
278	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile
279			115					120					125			
282	Ser	Ile	Ile	Asn	Glu	Asp	Gly	Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe
283		130					135					140				
286	Glu	Pro	Pro	Pro	Pro	Gly	Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro
287	145					150					155				160	
290	Phe	Ser	Ala	Phe	Ser	Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr
291				165					170						175	
294	Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met
295				180					185					190		
298	Lys	Ile	Asn	Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val
299			195					200					205			
302	Phe	Arg	Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly
303		210					215					220				
306	Val	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys
307	225					230					235				240	
310	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly
311				245					250						255	
314	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr
315				260					265					270		
318	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	Ala	Val	Gly
319			275					280					285			
322	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	Asp	Ala	Gln	Lys
323		290					295					300				
326	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp	Ser	Ser	Trp	Arg
327	305					310					315				320	
330	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Thr	Gly	Asn
331				325					330						335	
334	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Thr	Asn	Glu	Val
335				340				345					350			
338	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro
339			355					360					365			
342	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly
343		370					375					380				
346	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg
347	385					390					395				400	
350	Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile
351				405					410						415	
354	Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr
355				420					425					430		
358	Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala
359			435					440					445			
362	Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val
363		450					455					460				
366	Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu
367	465					470					475				480	

VERIFICATION SUMMARY

DATE: 08/30/2001

PATENT APPLICATION: US/09/806,703

TIME: 09:49:06

Input Set : A:\3631-109P.ST25.txt

Output Set: N:\CRF3\08302001\I806703.raw

L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:2070 M:283 W: Missing Blank Line separator, <220> field identifier
L:2101 M:283 W: Missing Blank Line separator, <220> field identifier
L:2166 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:2166 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2166 M:283 W: Missing Blank Line separator, <400> field identifier
L:2176 M:283 W: Missing Blank Line separator, <220> field identifier
L:2194 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:2194 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: